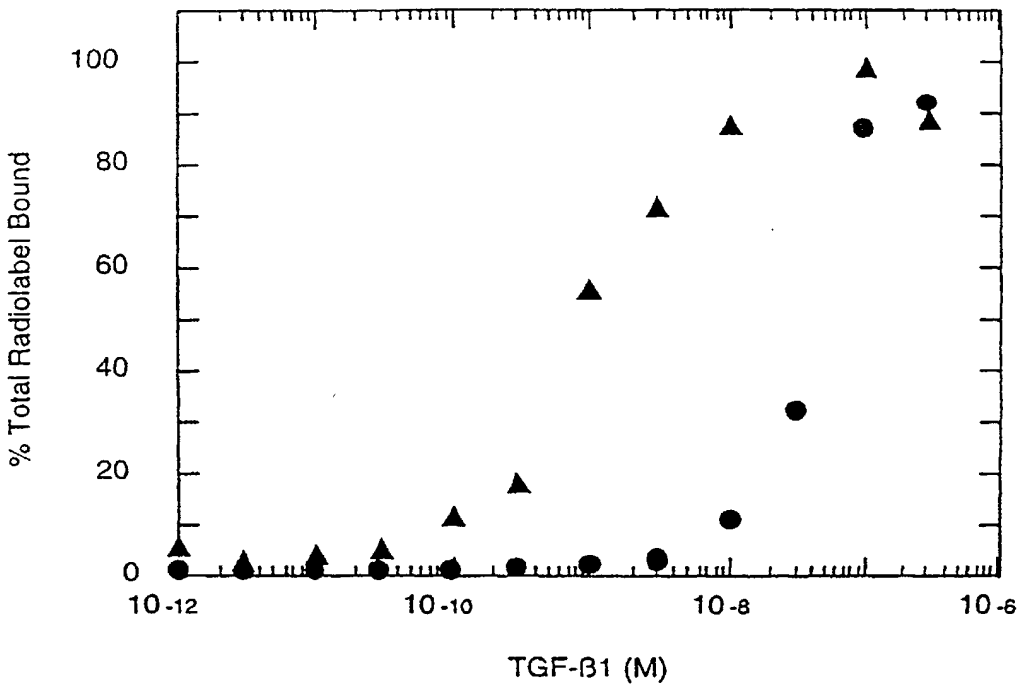

100
80
60
40
20
0
% Total Radiolabel Bound
10-12
10-10
10-8
10-6
TGF-β1 (M)

FIGURE 1

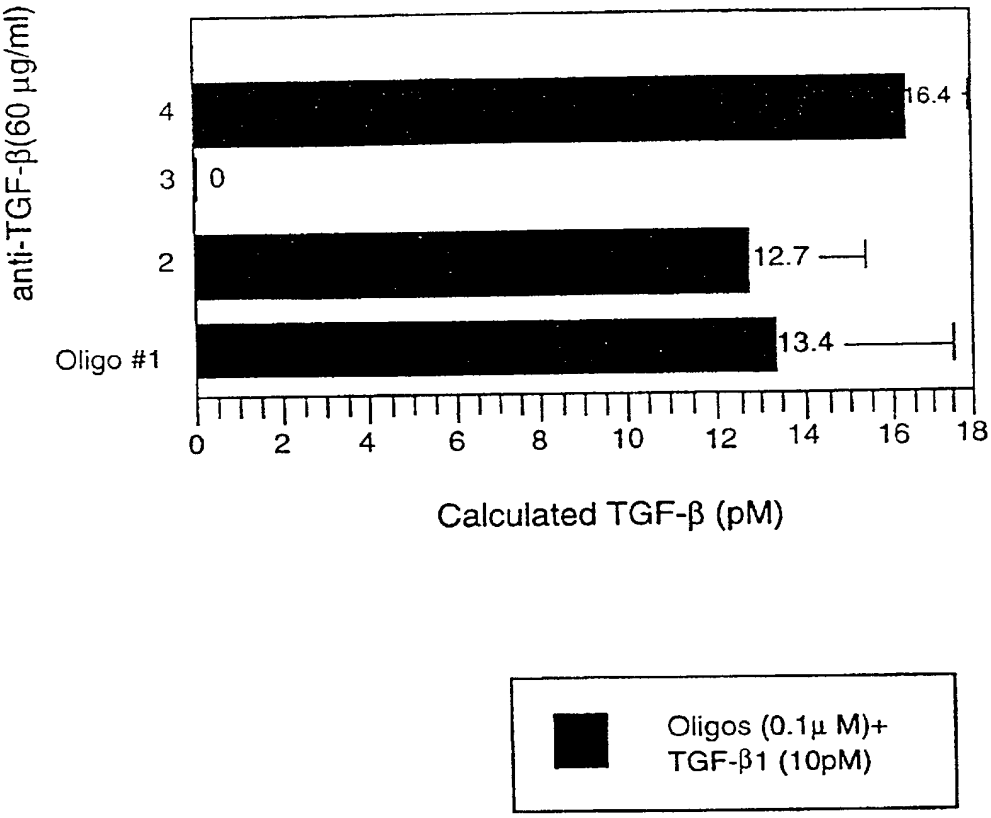
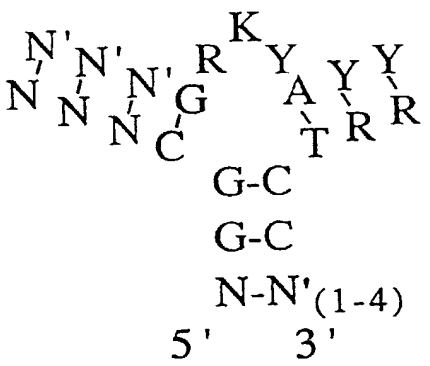

anti-TGF-β(60 µg/ml)
4
3
2
Oligo #1
16.4
0
12.7
13.4
0 2 4 6 8 10 12 14 16 18
Calculated TGF-β (pM)
Oligos (0.1µ M)+
TGF-β1 (10pM)

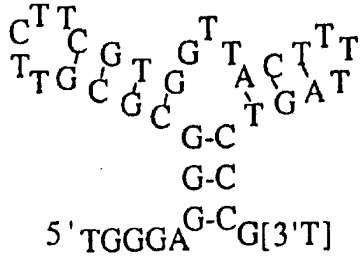
FIGURE 2



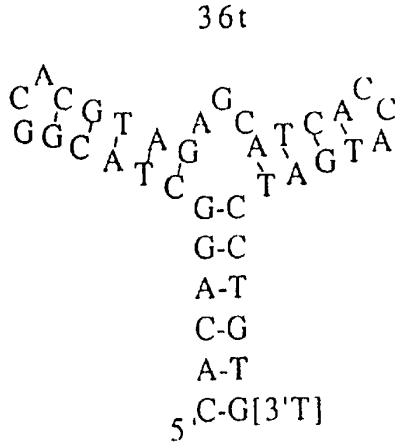
Helix I

SEQ ID NO: 171

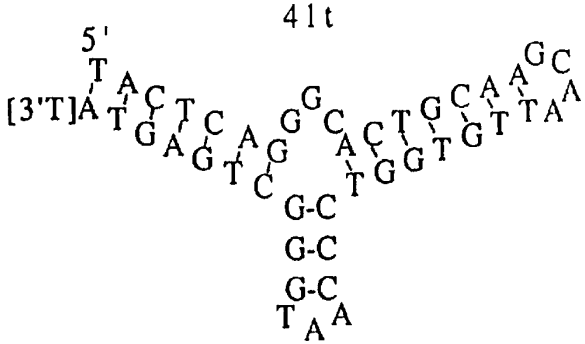
FIGURE 3



SEQ ID NO: 172



SEQ ID NO: 173



SEQ ID NO: 174

FIGURE 4

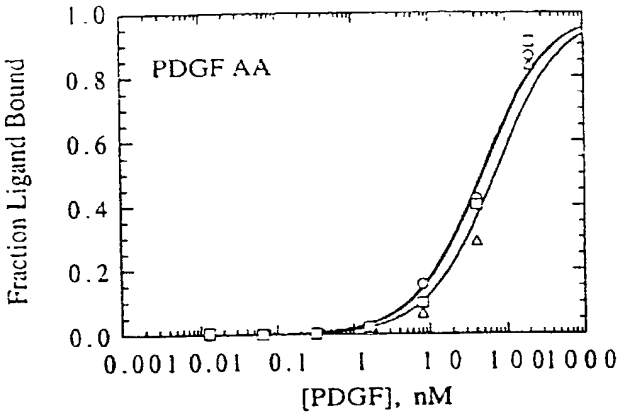


Figure 5A

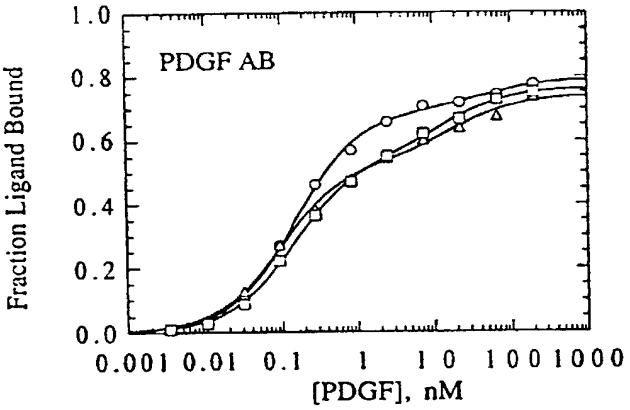


Figure 5B

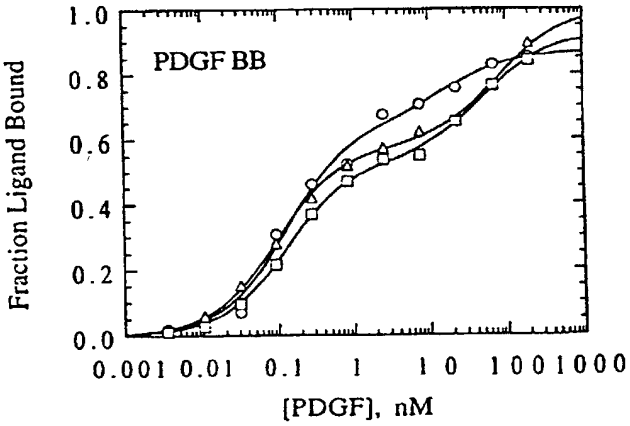


Figure 5C

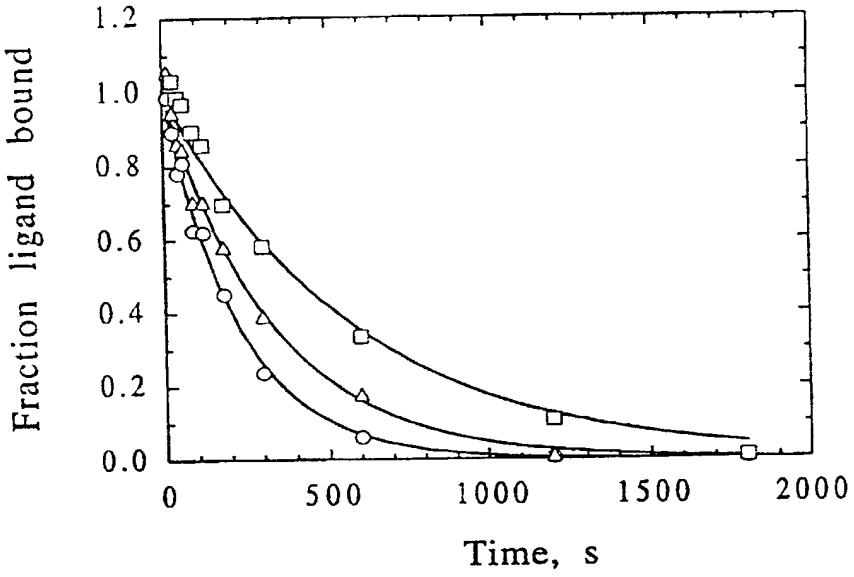

Fraction ligand bound
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
500
1000
1500
2000
Time, s

FIGURE 6

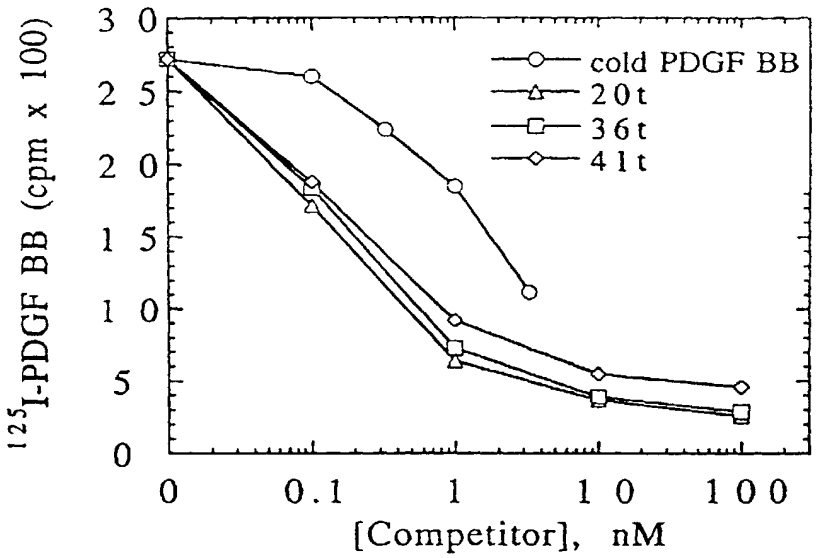

^{125}I-PDGF BB (cpm x 100)
30
25
20
15
10
5
0
0
0.1
1
10
100
[Competitor], nM
cold PDGF BB
20t
36t
41t

FIGURE 7

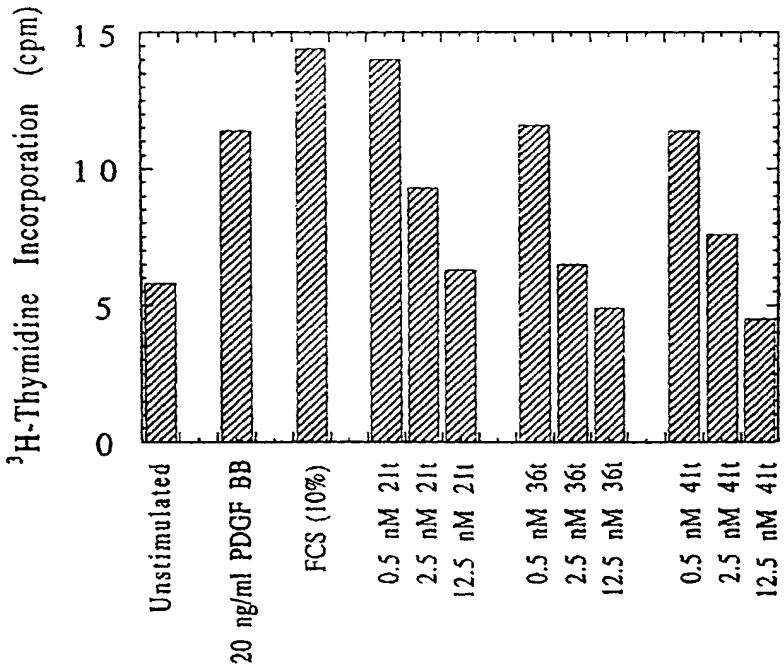
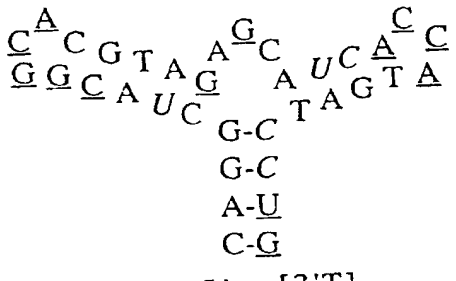
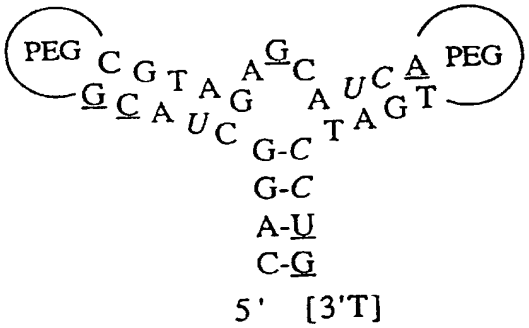

^{3}H-Thymidine Incorporation (cpm)
15
10
5
0
Unstimulated
20 ng/ml PDGF BB
FCS (10%)
0.5 nM 21t
2.5 nM 21t
12.5 nM 21t
0.5 nM 36t
2.5 nM 36t
12.5 nM 36t
0.5 nM 41t
2.5 nM 41t
12.5 nM 41t

FIGURE 8



K_d=0.065 nM

SEQ ID NO: 175



K_d=0.097 nM

SEQ ID NO: 176

FIGURE 9

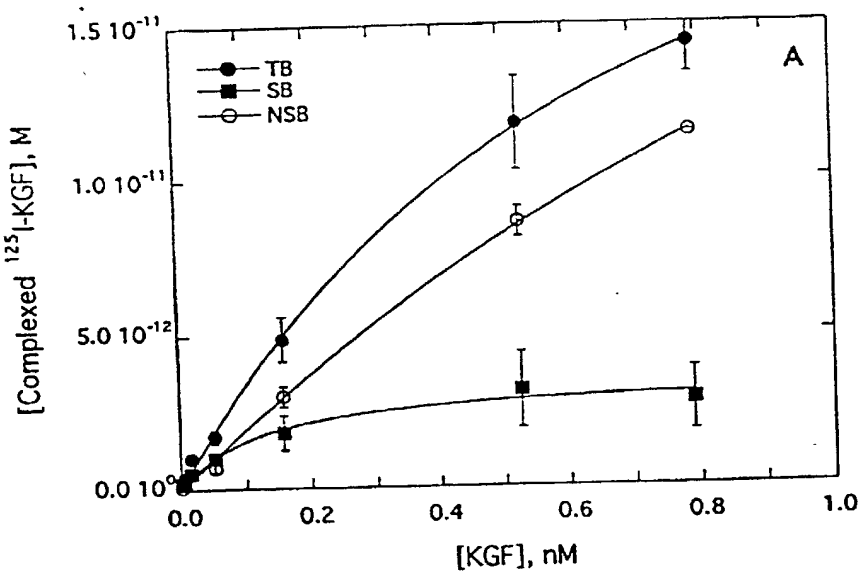

1.5 10^-11
1.0 10^-11
5.0 10^-12
0.0 10^0
[Complexed 125I-KGF], M
TB
SB
NSB
A
0.0
0.2
0.4
0.6
0.8
1.0
[KGF], nM

FIGURE 10A

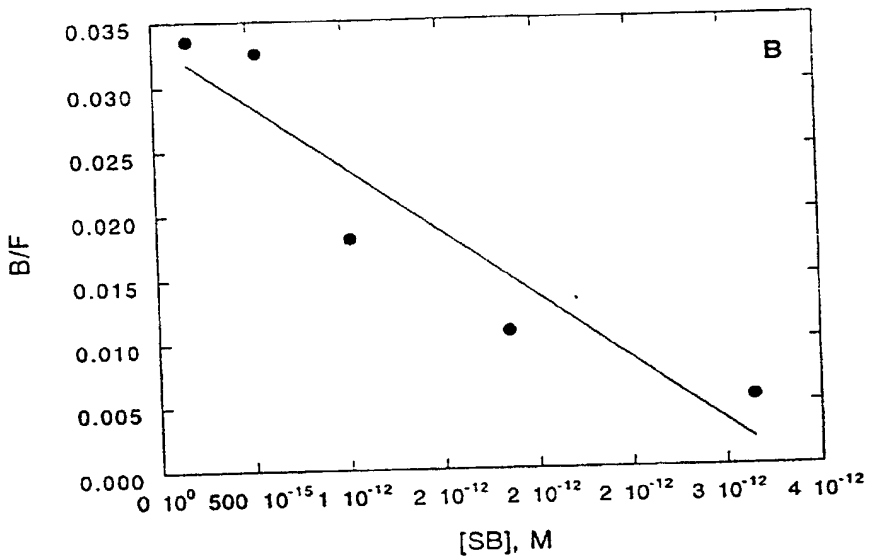

B
B/F
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0 10^0 500 10^-15 1 10^-12 2 10^-12 2 10^-12 2 10^-12 3 10^-12 4 10^-12
[SB], M

FIGURE 10B

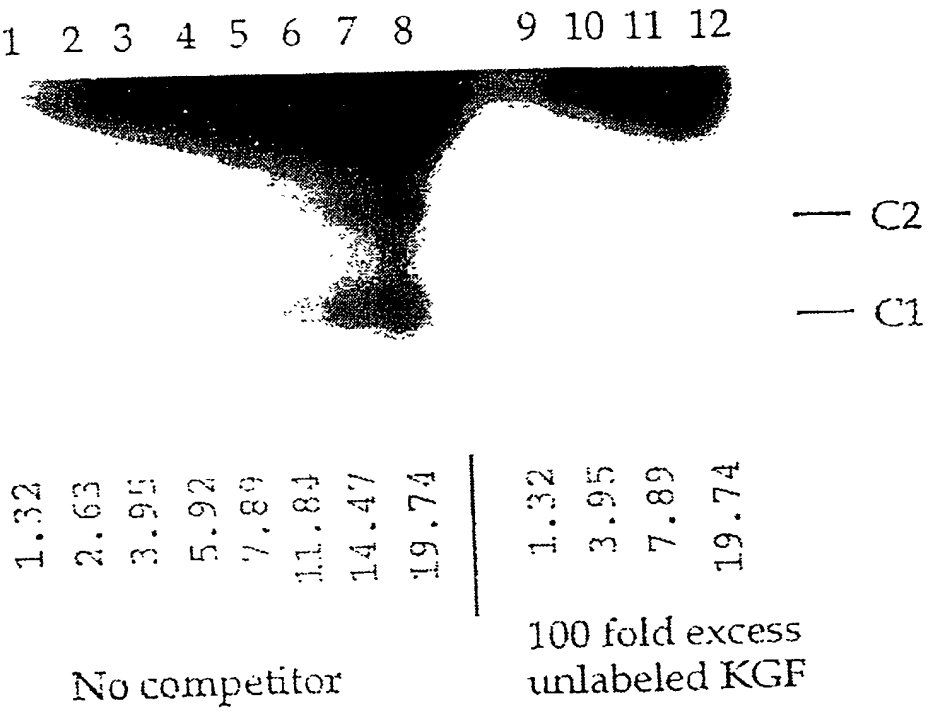

1 2 3 4 5 6 7 8 9 10 11 12
C2
C1
[125I-KGF], nM
1.32
2.63
3.95
5.92
7.89
11.84
14.47
19.74
No competitor
1.32
3.95
7.89
19.74
100 fold excess
unlabeled KGF

FIGURE 11

Class 1

SEQ ID NO:	Clone	K_d, nM	K_i, nM					
231	*14F	0.001	3.3	gggagg	acgaugcggUGG	UCUCCC	AAUUCUAAACUUUCU	CCAUCGUAUCUGGG
223	*6F	0.05	1.3	gggaggg	cgaugcggG	AUCCUUU	GUGGGCUCUUGUUGACCCC	CUCGUUGUCCCCCC
232	*15F	0.07	6.7	gggaggacg	augcggUCAUGG	UGUCUUUCC	ACAGCUCUUC	CCAUGAUCGCCCGG
259	*56F	0.07	0.3	gggaggacg	augcggGGACAAWYAGCGGUGUCUUUUC	AUUURKAUC	CUCCGACRUCCcag
240	*26F	0.23		AACAGUCUG	GCAAUGGCCAUUAUGGCGC	CCcagac	gacuc	gcccga
246	37F	0.46	6.7	acgaugcgg	GCCCGAUC	UACUGCAUU	ACCGAAAC	CAUUUCCCCACUCU
233	*16F	0.83		gggagg	gacgaugcggGAA	UUCCC	AGCGCUUGACUGAUACAAACN	UUCCCGUGCCCcag
249	42F	0.9		gggagg	acgaugcggCGACACAAUAGCCUUU	GAUCCCAUGAUGGCUCG	CCGUGCCcagacga
244	31F	1.0		gggaggacgaugcggAACGGAGAUG	UCCC	CUCAAMAUUUAC	CGUCUCCGUUUGCC
245	35F	1.1		gggagg	acgaugcggCGAAAU	UAGCUUCUU	AUGACUCAC	GUUUCCUUGCCGCC
257	54F	1.23		gggagg	acgaugcgg	AAGAUCUCCC	AACUGCUGUGGCUAAUAAUUCUCU	CCGCGUCCCcagac
255	51F	1.27		gggagg	acgaugcggCAG	UCUCCC	UAGGUUUCAU	CUCUGCAGCAUUCC
220	2F	1.77		gggaggacga	ugcggGCAUUCGUC	AAUACCUUGUUUUAUUCCUUUUCUAGCGCCca		gacgacuccgccga
239	24F	2.02		gggagg	acgaugcggUGG	UCUCCC	UAGAUCUACAGCACUU	CCAUCGCAUUGGGC
262	60F	2.1		gggagg	acgaugcgg	UGACAUGGAAUUUUCU	ACGGGCCCGAUCCUGCCAG	CCGUGUGcagacga
238	23F	2.52		gggaggg	cgaugcgg	CCCUACCACUUUUUCC	CUCUACUGUUA	UCCUGUC
222	5F	2.53		gggaggacg	augcggCGUCCCGAGUC	ACGCUGUCCU	GAUAACCUUCUCUGUGCCcagacgacucgcccga	
225	8F	2.63		gggaggacgaugcggUUUCGAAUAGGG	CCAUUUCUC	ACUAGCUA	UCCUACCCUGCCag	
243	29F	3.24		gggagg	acgaugcggGGA	CUUC	AACUAAGUCCUCAUUUGCCUCGC	UCCUCGUGCCcagga
224	7F	3.69		gggagg	acgaugcgg	CGGGUACUCUUC	GCCAGCUCCUCCAAGCGCgAC	CUGUGCCcagacga
252	45F	4.7		gggaggacga	ugcggGUCGU	AUUCAUCUCCUUGUUCUGUUUCGUUGCACCUGGCCcag		acgacucgccga
268	Consensus			gGgagg	Sgagg	uYucYy	RRYuy	yYsYs

Summary Structure

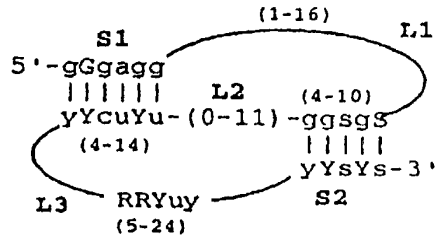


FIGURE 12A

Class 2

SEQ ID NO:	Clone	K_d, nM	K_i, nM					
230	*13F	0.03	10.0	ggacgauacgg	CACCUUAGACCUGUCCUCCAAGCGUGAGUUG		CUGUGGCCcaga	cgacucgccg
254	*50F	0.12		cgauacgaUGA	UCAAUC	GGCGCU	UUACUCUUGCUCUCACC	GUGCCCcagac
247	38F	0.33	0.2	ggaggacgaug	cggNGACUGAUUUUUCCUUG	NCAGUGUA	AUUUCCUG	GCUGCCCcaga
227	10F	0.47	10.0	gggagg	acgaugcggGACCAGA	UGGCGGA	UUUUUCAGCAAUCCUCCCCCGCUGCCcag	
226	9F	0.83		ggacgauacgg	AUAAUGGCUAGA	ACUAGC	UCGCAUC	UUGGUGUCCGG
256	53F	0.7		gggag	gacgaugcggAUCAAA	AGCACUCA	UUCCC	GUGCUCGCUUC
253	49F	1.0		gaggacgauac	ggGGACU	UUGACAG	GCAUUGAUU	UCGACGUGUUC
250	43F	1.13	16.7	gggag	gacg	augcggUGUAG	UUUCC	CUCUAUGCCAU
260	57F	1.2		ggacgaugcgg	UGACUAUCU	GGCUCGAU	CCAAUCACC	CGAGCCCACCG
248	41F	1.44		ggaggacgaug	cggGGACUUU	GACAGG	CAUUGAUUUCGA	CCUCUUCCCCG
241	27F	1.52		ggaggacgaug	cggCAGUC	UGGAUCUC	UAUUGGA	AUUUAGUCCUC
235	20F	2.05		ugcggAGUA	UUCCAGCCUGGAUUCAU	AGUCAG	UGCUCUCCGUGCCcagacgacucgcc	
258	55F	2.52		gggag	gacgaugcggUCCGUCAUAAC	GGCCAUAAACUGCGAAUA	CUCCC	UGGCCcagacg
261	58F	2.52		gggagg	acgaugcggGAACUAA	UGGCCGUGAUUAACCAAUGCAGG	CUUCC	UGCGCcagacg
221	3F	4.47		gggaggacgaugcggAUCGUAAUC		GCCACUACUA	CUUUCCGAACCCGCAC	CUGCCcagacg
236	21F	ND		gggaggacg	augcggUCCUA	GCAGCGAUUCAUCCC	CGUUCUCUCAG	CGUUGCCCCca
242	28F	ND		gggagga	cgaugcggGAUUCU	UUCGGCAAGUCAAAAAUA	UCCUU	GCUUCCCGAGC
269	Consensus			rgGrrg	RaYY	rsBrs	YyyYyb	syBsY

Summary Structure

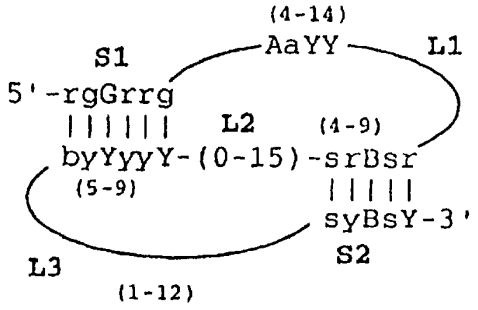
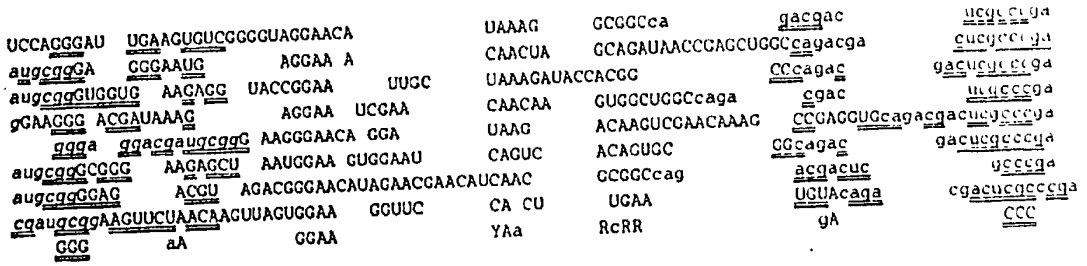


FIGURE 12B

Class 1

SEQ ID NO:	Clone	Kd, nM	Ki, nM
195	14N	0.4	2.0
199	25N	0.9	
191	4N	0.7	23.3
189	1N	0.5	16.7
205	36N	8.27	
203	34N	0.8	
207	42N	0.8	266.7
196	16N	1.4	
	Consensus		

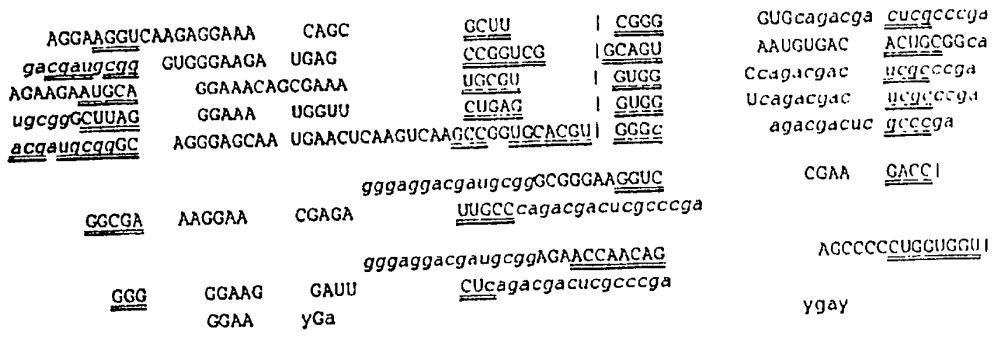


Summary Structure

FIGURE 12C

Class 2

SEQ ID NO	Clone	Kd, nM	Ki, nM
209	47N	1.8	
198	24N	1.2	
202	29N	0.43	13.3
204	35N	2.3	
192	6N	0.7	26.7
190	2N	0.8	66.7
211	54N	5.3	
271	Consensus		



Summary Structure

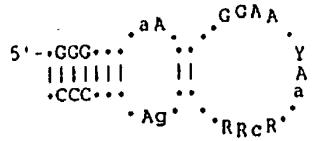


FIGURE 12D

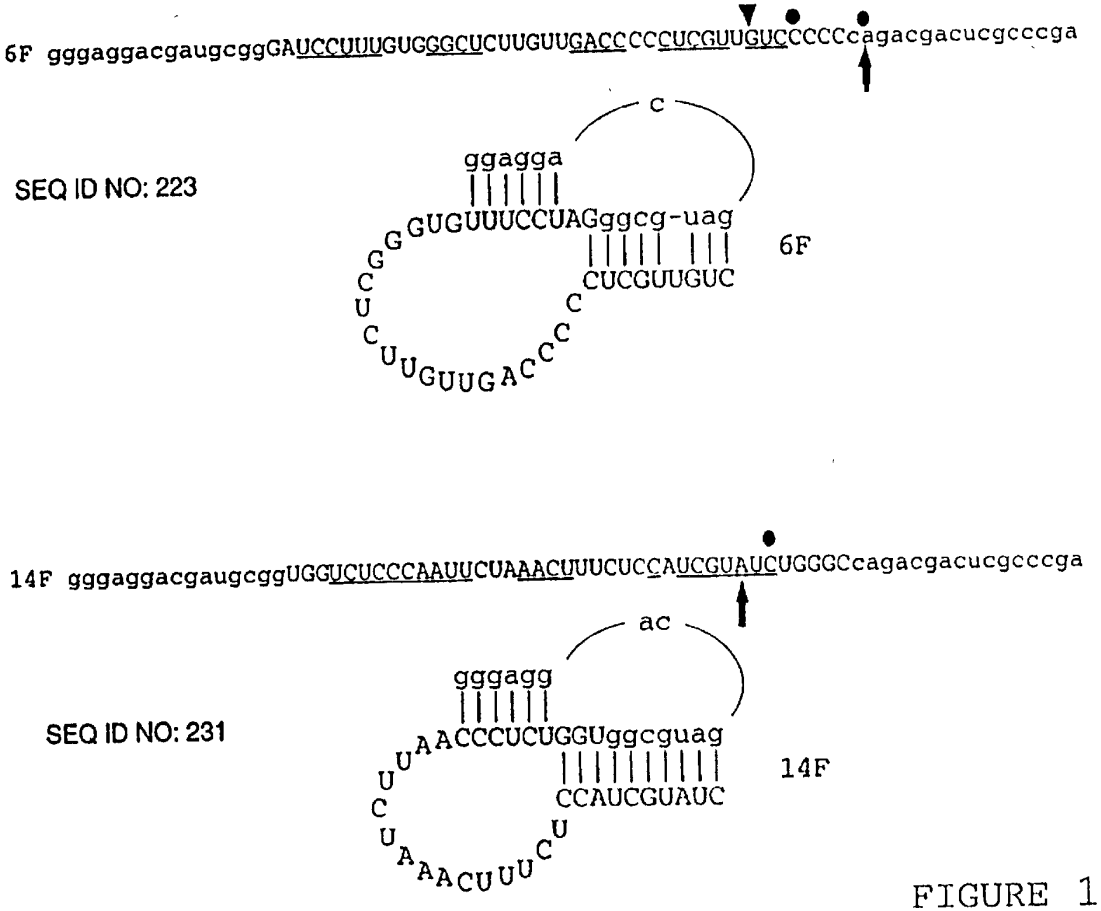

6F gggaggacgaugcggGAUCCUUUGUGGGCUCUUGUUGACCCCCUCGUUGUCCCCCcagacgacucgcccga
SEQ ID NO: 223
c
ggagga
GUGUUUCCUAGggcg-uag
6F
CUCGUUGUC
14F gggaggacgaugcggUGGUCUCCCCAAUUCUAAACUUUCUCCAUCGUAUCUGGGCcagacgacucgcccga
SEQ ID NO: 231
ac
gggagg
AACCCUCUGGUggcguag
14F
CCAUCGUAUC

FIGURE 13